



SEQUENCE LISTING

<115> Vander Horn, Peter B.

Wang, Yan

MJ Bioworks, Incorporated

<120> Novel Compositions With Polymerase Activity

<130> 020130-001510US

<140> US 10/627,582

<141> 2003-07-25

<150> US 60/398,687

<151> 2002-07-25

<150> US 60/483,287

<151> 2003-06-27

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<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:full-length
assembled hybrid polymerase clone Phyl

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<210> 2

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:full-length
assembled hybrid polymerase clone Phyl

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Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu His Asp Arg
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Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
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Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
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Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
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Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
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```

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
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Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
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Ser Tyr Ala Asp Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
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Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
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Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
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Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	245	250	255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Arg	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270
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Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Lys	Ala	Trp	Glu	Thr	Gly	Glu	Gly	290	295	300
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Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350
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 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
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 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
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 Tyr Asp Pro Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
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 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:PhS1, Phyl and SSo7d fusion protein

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PhS1, Phyl and
SSo7d fusion protein

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Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu His Asp Arg
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Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
  35               40               45

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Glu	Leu	Gly	Lys	Glu	Phe	Phe	Pro	Met	Glu	Ala	Gln	Leu	Ser	Arg	Leu	325	330	335
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Pro	Asn	Lys	Pro	Asp	Glu	Arg	Glu	Tyr	Glu	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380
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His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Arg	Asn	Tyr	420	425	430
Asp	Val	Ala	Pro	Glu	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Pro	Gly	435	440	445
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Lys	Lys	Tyr	Ala	Leu	Ile	Asp	Glu	Glu	Gly	Lys	Ile	Ile	Thr	Arg	Gly	595	600	605
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Ala	Arg	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asn	Val	Glu	Glu	Ala	625	630	635
Val	Arg	Ile	Val	Lys	Glu	Val	Thr	Gln	Lys	Leu	Ser	Lys	Tyr	Glu	Ile	645	650	655
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His	660	665	670
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Arg	Leu	Ala	675	680	685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

Tyr Asp Pro Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ser
755 760 765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
770 775 780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785 790 795 800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
805 810 815

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<211> 2535

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:hybrid
polymerase Sso7d fusion protein PhS2

<400> 5

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aagaaagtat ggcgtgtggg caagatgac tccttcacct acgacgaggg cggtggcaag 2460
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<210> 6

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase Sso7d fusion protein PhS2

<400> 6

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Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
      20               25               30

```

```

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
      35               40               45

```

```

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
      50               55               60

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```

Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Lys Pro Ile
      65               70               75               80

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Glu Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
      85               90               95

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Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
     100               105               110

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Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
     115               120               125

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Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
     130               135               140

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Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Gly	Lys	Gly	Pro	Ile	Ile	Met	Ile	145	150	155	160
Ser	Tyr	Ala	Asp	Glu	Asn	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Lys	Ile	165	170		175
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	180	185		190
Arg	Phe	Leu	Lys	Val	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Ile	Ile	Val	Thr	195	200		205
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Phe	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu	210	215		220
Lys	Leu	Gly	Ile	Lys	Leu	Pro	Ile	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230		235
Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	245	250		255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Arg	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265		270
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	275	280		285
Lys	Val	Tyr	Ala	His	Glu	Ile	Ala	Glu	Ala	Trp	Glu	Ser	Gly	Glu	Gly	290	295		300
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr	305	310		315
Glu	Leu	Gly	Lys	Glu	Phe	Phe	Pro	Met	Glu	Ile	Gln	Leu	Ser	Arg	Leu	325	330		335
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345		350
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Leu	Ala	355	360		365
Pro	Asn	Lys	Pro	Ser	Glu	Arg	Glu	Tyr	Glu	Arg	Arg	Leu	Arg	Glu	Ser	370	375		380
Tyr	Thr	Gly	Gly	Tyr	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asn	385	390		395
Ile	Val	Tyr	Leu	Asp	Phe	Arg	Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410		415
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Leu	Glu	Gly	Cys	Lys	Glu	Tyr	420	425		430
Asp	Val	Ala	Pro	Glu	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Ile	Pro	Gly	435	440		445
Phe	Ile	Pro	Ser	Leu	Leu	Gly	His	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Ile	450	455		460

Lys	Arg	Lys	Met	Lys	Ala	Ser	Lys	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu	465	470	475	480
Asp	Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Phe	Tyr	Gly	485	490		495
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	500	505		510
Ser	Val	Thr	Ala	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Leu	Val	Arg	Lys	Glu	515	520		525
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly	530	535		540
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Lys	Ser	Glu	Glu	Ile	Lys	Lys	Lys	545	550	555	560
Ala	Leu	Glu	Phe	Val	Asp	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu	565	570		575
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	580	585		590
Lys	Arg	Tyr	Ala	Leu	Ile	Asp	Glu	Glu	Gly	Lys	Ile	Ile	Thr	Arg	Gly	595	600		605
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	610	615	620	
Ala	Lys	Val	Leu	Glu	Thr	Ile	Leu	Lys	His	Gly	Asn	Val	Glu	Glu	Ala	625	630	635	640
Val	Arg	Ile	Val	Lys	Glu	Val	Thr	Gln	Lys	Leu	Ala	Lys	Tyr	Glu	Ile	645	650		655
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Pro	Pro	Leu	His	660	665		670
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Arg	Leu	Ala	675	680		685
Ala	Arg	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val	690	695	700	
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu	705	710	715	720
Tyr	Asp	Leu	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn	725	730		735
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Ala	Phe	Gly	Tyr	Arg	740	745		750
Lys	Glu	Asp	Leu	Arg	Tyr	Gln	Lys	Thr	Lys	Gln	Val	Asp	Leu	Thr	Ala	755	760	765	
Cys	Leu	Asn	Ile	Lys	Lys	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Ala	Thr	Val	770	775	780	

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785 790 795 800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
805 810 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
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Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
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<210> 7

<211> 2535

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase Sso7d fusion protein PhS5

<400> 7

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accgtgtgga gactgtattt cgaacatcca caagatgttc cggctattcg cgataaagtt 300
cgcgaaacatc ctgcagttgt tgacatcttc gaatacgata ttccatttgc aaagcgttac 360
ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagct cctggcgcttc 420
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<210> 8
<211> 844
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein PhS5

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      20             25             30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
      35             40             45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
      50             55             60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
      65             70             75             80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
      85             90             95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
      100            105            110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
      115            120            125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
      130            135            140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
      145            150            155            160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
      165            170            175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
      180            185            190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
      195            200            205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
      210            215            220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
      225            230            235            240

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Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Ile	Lys	Gly	Arg	Ile		
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His	Phe	Asp	Leu	Tyr	His	Val	Ile	Thr	Arg	Thr	Ile	Asn	Leu	Pro	Thr		
			260					265					270				
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu		
		275					280					285					
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Glu	Ala	Trp	Glu	Ser	Gly	Lys	Asn		
	290					295					300						
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr		
305					310					315					320		
Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ile	Gln	Leu	Ser	Arg	Leu		
				325					330					335			
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu		
			340					345					350				
Val	Glu	Trp	Tyr	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Val	Ala		
		355					360					365					
Pro	Asn	Lys	Pro	Asp	Glu	Glu	Glu	Tyr	Glu	Arg	Arg	Leu	Arg	Glu	Ser		
	370					375					380						
Tyr	Thr	Gly	Gly	Tyr	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asn		
385					390					395					400		
Leu	Val	Ser	Leu	Asp	Phe	Arg	Ala	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr		
				405					410					415			
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Lys	Glu	Tyr		
			420					425					430				
Asp	Ile	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Pro	Gly		
	435						440					445					
Phe	Ile	Pro	Ser	Leu	Leu	Lys	His	Leu	Leu	Asp	Glu	Arg	Gln	Glu	Ile		
	450					455					460						
Lys	Arg	Lys	Met	Lys	Ala	Ser	Lys	Asp	Pro	Ile	Glu	Lys	Lys	Met	Leu		
465					470				475						480		
Asp	Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Phe	Tyr	Gly		
				485				490					495				
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu		
		500						505					510				
Ser	Val	Thr	Ala	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Leu	Val	Trp	Lys	Glu		
		515					520					525					
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly		
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Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Lys	Pro	Glu	Glu	Ile	Lys	Lys	Lys		
545					550					555					560		

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
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 Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
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 Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
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 705 710 715 720
 Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
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<210> 9
 <211> 2535
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase Sso7d fusion protein PhS7

<400> 9

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gtggctgttg caaagagact ggctgctaga ggcgtgaaag ttagaccggg tatggtaatt 2100
ggctacattg tactccgcgg cgatggctcg attagcaacc gtgcaattct agctgaggaa 2160
tacgatctga aaaagcacia gtatgacgca gaatattaca ttgagaacca ggtgctcccg 2220
gcggtactcc gtattctgga ggcttttggc taccgtaagg aagacctccg ctggcaaaag 2280
actaaacagg ttggcctcac ttcttggtc aacattaaaa aatccggtac cggcggtggc 2340
ggtgcaaccg taaagttcaa gtacaaaggc gaagaaaaag aggtagacat ctccaagatc 2400
aagaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cgggtggcaag 2460
accggccgtg gtgcggtgaa cgaaaaggac gcgccgaagg agctgctgca gatgctggag 2520
aagcagaaaa agtga 2535
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<210> 10

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase Sso7d fusion protein PhS7

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Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
35 40 45
Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60
Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80
Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
85 90 95
Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125
Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
130 135 140
Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
165 170 175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190
Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
195 200 205
Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220
Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
245 250 255
His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260 265 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
290 295 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
 355 360 365
 Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
 420 425 430
 Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly Arg Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460
 Lys Thr Lys Met Lys Ala Thr Lys Asp Pro Ile Glu Lys Lys Leu Leu
 465 470 475 480
 Asp Tyr Arg Gln Lys Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Phe Val Arg Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640

Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
675 680 685

Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
755 760 765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
770 775 780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785 790 795 800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
805 810 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
820 825 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
835 840

<210> 11
<211> 2337
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
polymerase Hyb1

<220>
<221> modified_base
<222> (1416)
<223> n = g, a, c or t

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ctgctgagag atgattctaa gattgaggaa gttagaaaaa tcactgctga gcgccatggc 180
aagattgttc gtatcggttg tgtggaaaag gtaaggaaga aatttctggg cagaccaatc 240
aaggtgtgga gactgtatct cgaacatcca caagatgttc cgactattcg cgataaagtt 300
cgcgaaacatc ctgcagttat tgacatcttc gaatacgata ttgcatttgc aaagcgttac 360

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ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagat cctggcggttc 420
gatatagaaa ccctctatca cggaagcgaa gagtttggtg aaggcccaat tataatgatc 480
agctatgcag atgaaaacga agcaaagggtg attacttgga aaaacataga tctcccatac 540
gttgagggtg tatcttccga gcgcgagatg attaaacgct ttctcagaat tatccgcgag 600
aaggatccgg acattatcgt tacttataac ggcgactctt ttgacctccc atatctggcg 660
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aagttctgca aggacttcct tggctttatt ccgtctctcc tggggcatct gctcgaggaa 1380
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gctctagaat ttgtgaaata cattaactcg aagctccccg gtctcttgga gctcgaatat 1740
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gaaggcaaaa ttattactcg tggctcgcag attgtgcgcc gtgattggag cgaaattgag 1860
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ctcgcgattt atgagcagat tactcgcccc ctgcatgagt ataaggcgat tggctccgac 2040
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gcggtactcc gtattctgga gggttttggc taccgtaagg aagacctccg ttggcaaaag 2280
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<210> 12
<211> 775
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:hybrid
polymerase Hyb1

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<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

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Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
      20             25             30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
      35             40             45

Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
      50             55             60

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Ile	Val	Asp	Val	Glu	Lys	Val	Arg	Lys	Lys	Phe	Leu	Gly	Arg	Pro	Ile	
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Lys	Val	Trp	Arg	Leu	Tyr	Phe	Glu	His	Pro	Gln	Asp	Val	Pro	Thr	Ile	
				85					90					95		
Arg	Asp	Lys	Val	Arg	Glu	His	Pro	Ala	Val	Ile	Asp	Ile	Phe	Glu	Tyr	
			100					105					110			
Asp	Ile	Ala	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	
		115					120					125				
Met	Glu	Gly	Glu	Glu	Glu	Leu	Lys	Ile	Leu	Ala	Phe	Asp	Ile	Glu	Thr	
	130					135					140					
Leu	Tyr	His	Gly	Ser	Glu	Glu	Phe	Gly	Lys	Gly	Pro	Ile	Ile	Met	Ile	
145					150					155					160	
Ser	Tyr	Ala	Asp	Glu	Asn	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Asn	Ile	
				165				170						175		
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	
			180					185					190			
Arg	Phe	Leu	Arg	Ile	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Ile	Ile	Val	Thr	
		195					200					205				
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Leu	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu	
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Lys	Leu	Gly	Ile	Lys	Leu	Thr	Leu	Gly	Arg	Asp	Gly	Cys	Glu	Ala	Lys	
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Met	Gln	Arg	Leu	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	
				245				250						255		
His	Phe	Asp	Leu	Tyr	Tyr	Val	Ile	Ser	Arg	Thr	Ile	Asn	Leu	Pro	Thr	
			260					265					270			
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	
		275					280					285				
Lys	Val	Tyr	Ala	Asp	Asp	Ile	Ala	Glu	Ala	Trp	Glu	Thr	Gly	Lys	Gly	
	290					295					300					
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr	
305					310					315					320	
Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ala	Gln	Leu	Ser	Arg	Leu	
				325					330					335		
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	
			340					345					350			
Val	Glu	Trp	Tyr	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Val	Ala	
		355					360					365				
Pro	Asn	Lys	Pro	Tyr	Glu	Arg	Glu	Tyr	Glu	Arg	Arg	Leu	Arg	Glu	Ser	
	370					375					380					

Tyr	Thr	Gly	Gly	Phe	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Ser	
385					390					395					400	
Leu	Val	Ser	Leu	Asp	Phe	Arg	Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	
				405					410						415	
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Lys	Asp	Tyr	
			420					425						430		
Asp	Ile	Ala	Pro	Glu	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Leu	Gly	
		435					440						445			
Phe	Ile	Pro	Ser	Leu	Leu	Gly	His	Leu	Leu	Glu	Glu	Arg	Gln	Glu	Ile	
	450					455						460				
Lys	Thr	Lys	Met	Lys	Glu	Thr	Xaa	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu	
465					470					475					480	
Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Tyr	Tyr	Gly	
				485					490						495	
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	
			500					505						510		
Ser	Val	Thr	Ala	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Phe	Val	Trp	Lys	Glu	
		515					520						525			
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly	
	530					535						540				
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Glu	Pro	Glu	Glu	Ile	Lys	Lys	Lys	
545					550					555					560	
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu	
				565					570						575	
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	
			580					585						590		
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Ile	Ile	Thr	Arg	Gly	
		595					600						605			
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	
	610					615						620				
Ala	Lys	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asn	Val	Glu	Glu	Ala	
625					630					635					640	
Val	Lys	Ile	Val	Lys	Glu	Ile	Ile	Glu	Lys	Leu	Ala	Lys	Tyr	Glu	Ile	
				645					650						655	
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His	
			660					665						670		
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala	
		675					680					685				
Ala	Arg	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val	
	690					695						700				

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
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 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
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<210> 13
 <211> 2535
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase Hyb1-Sso7d fusion protein HyS1

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 <221> modified_base
 <222> (1416)
 <223> n = g, a, c or t

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 ctgctgagag atgattctaa gattgaggaa gttagaaaaa tcaactgctga gcgccatggc 180
 aagattgttc gtatcggtga tgtggaaaag gtaaggaaga aatttctggg cagaccaatc 240
 aaggtgtgga gactgtattt cgaacatcca caagatgttc cgactattcg cgataaagtt 300
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 gatatagaaa ccctctatca cggaagcgaa gagtttggtg aaggcccaat tataatgatc 480
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<210> 14
<211> 844
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:hybrid
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<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

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  1             5             10             15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
      20             25             30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
      35             40             45

Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
      50             55             60

Ile Val Asp Val Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
      65             70             75             80

Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
      85             90             95

Arg Asp Lys Val Arg Glu His Pro Ala Val Ile Asp Ile Phe Glu Tyr
      100            105            110

Asp Ile Ala Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
      115            120            125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
      130            135            140

Leu Tyr His Gly Ser Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
      145            150            155            160

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Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Thr Leu Gly Arg Asp Gly Cys Glu Ala Lys
 225 230 235 240
 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr Tyr Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Asp Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
 355 360 365
 Pro Asn Lys Pro Tyr Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Ser
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
 420 425 430
 Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480

Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Tyr	Tyr	Gly	
				485					490						495	
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	
			500					505					510			
Ser	Val	Thr	Ala	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Phe	Val	Trp	Lys	Glu	
		515					520					525				
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly	
	530					535					540					
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Glu	Pro	Glu	Glu	Ile	Lys	Lys	Lys	
545					550					555					560	
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu	
				565					570					575		
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	
			580					585					590			
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Ile	Ile	Thr	Arg	Gly	
		595					600						605			
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	
	610					615					620					
Ala	Lys	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asn	Val	Glu	Glu	Ala	
625					630					635					640	
Val	Lys	Ile	Val	Lys	Glu	Ile	Ile	Glu	Lys	Leu	Ala	Lys	Tyr	Glu	Ile	
				645					650					655		
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His	
			660					665					670			
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala	
		675					680					685				
Ala	Arg	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val	
	690					695					700					
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Lys	Arg	Ala	Ile	Leu	Ala	Glu	Glu	
705					710					715					720	
Phe	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn	
			725						730					735		
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Gly	Phe	Gly	Tyr	Arg	
			740					745					750			
Lys	Glu	Asp	Leu	Arg	Trp	Gln	Lys	Thr	Lys	Gln	Ala	Gly	Leu	Thr	Ala	
		755					760					765				
Trp	Leu	Asn	Ile	Lys	Lys	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Ala	Thr	Val	
	770					775						780				
Lys	Phe	Lys	Tyr	Lys	Gly	Glu	Glu	Lys	Glu	Val	Asp	Ile	Ser	Lys	Ile	
785					790					795					800	

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
805 810 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
820 825 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
835 840

<210> 15
<211> 2340
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:truncated
hybrid polymerase Hyb2

<220>
<221> modified_base
<222> (1416)
<223> n = g, a, c or t

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ctgctggaag atgattctaa gattgatgaa gttagaaaaa tcaactgctga gcgccatggc 180
aagattgttc gtatcgttga tgcggaaaag gtagagaaga aatttctggg cagaccaatc 240
acggtgtgga aactgtattt cgaacatcca caagatgttc cgactattcg cgagaaaatt 300
cgcgaacatt ctgcagttgt tggcatcttc gaatacgata ttccatttgc aaagagttac 360
ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagct cctggcgttc 420
gatatagaaa cctctatca cgaaggcgaa gagtttgcta aaggcccaat tataatgac 480
agctatgcag atgaagacga agcaaagggtg attacttgga aaaaaataga tctcccatac 540
gttgagggtt tatcttccga gcgcgagatg attaagcgct ttctcagagt tatccgcgag 600
aaggatccgg acgttatcgt tacttataac ggcgactctt ttgacctccc atatctggcg 660
aaacgcgcag aaaaactcgg tattaactcg cctctcggcc gtgatgggtc cgagccgaag 720
atgcagcgtc tcggcgatat gaccgctgta gaagttaagg gtcgtatcca ttctgacctg 780
tatcatgtaa ttagccgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840
gcaatttttg gtaagccgaa ggagaaggta tacgccgatg agattgcagg ggcgtgggaa 900
accggtgagg acctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggcgatttat 960
gaactcggca aagaattctt cccaatggaa gttcagctcc ctgcctgggt tggccaacca 1020
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gcgtacgaac gcaacgaact ggctccgaac aagccagccg aacaagagta tgaacgccgt 1140
ctccgcgagt ctactactgg tggctttggt aaagagccag aaaagggcct ctgggaagac 1200
ctcgtgtccc tcgattttcg cgctctgtat ccgtctatta tcattaccca caacgtgtct 1260
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cgccaagaga ttaagaccaa aatgaaggag acccangatc cgattgaaaa aatactgctc 1440
gactatcgcc aaaaagcgat taaactcctc gcaaactctt attacggcta ttatggctat 1500
gcaaaagcac gctggtactg taaggagtgt gctgagtcgg ttactgcttg gggctcgcga 1560
tacatcgagt tcgtgtggaa ggagctcgaa gaaaagtttg gctttaaagt tctctacatt 1620
gacactgatg gtctctatgc gactattccg ggtggtgagc ctgaggaaat taagaaaaag 1680
gctctagaat ttgtgaaata cattaactcg aagctccccg gtctcttgga gctcgaatat 1740
gaaggctttt ataagcgcgg cttcttcggt accaagaaga gatatgcggt gattgatgaa 1800
gaaggcaaaa ttattactcg tggctctcag attgtgcgcc gtgattggag cgaaattgcg 1860
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ctcgcgattt atgagcagat tactcgcccc ctgcatgagt ataaggcgat tggctccgcac 2040
gtggctgttg caaagaaact ggctgctaga ggcgtgaaaa ttaaaccggg tatggtaatt 2100
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ttcgatctga gaaagcacia gtatgacgca gaattattaca ttgagaacca ggtgctccc 2220
 gcggactacc gtattctgga gggttttggc taccgtaagg aagacctccg ttagcaaaaag 2280
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<210> 16
 <211> 757
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:truncated
 hybrid polymerase Hyb2

<220>
 <221> MOD_RES
 <222> (472)
 <223> Xaa = unknown amino acid

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 Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
 35 40 45
 Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
 355 360 365
 Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
 420 425 430
 Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg
 755

<210> 17
 <211> 2340
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:truncated
 hybrid polymerase Hyb3

<220>
 <221> modified_base
 <222> (1416)
 <223> n = g, a, c or t

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 ctgctggaag atgattctaa gattgatgaa gttagaaaaa tcaactgctga gcgccatggc 180

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aagattgttc gtatcgttga tgcggaaaag gtagagaaga aatttctggg cagaccaatc 240
acgggtgtgga aactgtattt cgaacatcca caagatgttc cgactattcg cgagaaaatt 300
cgcgaacatt ctgcagttgt tggcatcttc gaatacgata ttccatttgc aaagagttac 360
ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagct cctggcgttc 420
gatatagaaa cctctatca cgaaggcgaa gagtttgcta aaggcccaat tataatgac 480
agctatgcag atgaagacga agcaaaggtg attacttgga aaaaaataga tctcccatac 540
gttgagggtt tatcttccga gcgcgagatg attaagcgct ttctcagagt tatccgcgag 600
aaggatccgg acgttatcgt tacttataac ggcgactctt ttgacctccc atatctggcg 660
aaacgcgcag aaaaactcgg tattaaactg cctctcggcc gtgatgggtc cgagccgaag 720
atgcagcgtc tcggcgatat gaccgctgta gaagttaagg gtcgtatcca ttctgacctg 780
tatcatgtaa ttagccgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840
gcaatttttg gtaagccgaa ggagaaggta tacgccgatg agattgcagg ggcgtgggaa 900
accggtgagg acctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggcgatttat 960
gaactcggca aagaattctt cccaatggaa gttcagctcc ctgcctgggt tggccaacca 1020
ctgtgggatg tttctcgttc ttccaccggg aacctcgtag agtggttgct cctgcgcaaa 1080
gcgtacgaac gcaacgaact ggctccgaac aagccagccg aacaagagta tgaacgccgt 1140
ctccgcgagt cttacactgg tggctttgtt aaagagccag aaaagggcct ctgggaagac 1200
ctcgtgtccc tcgattttcg cgctctgtat ccgtctatta tcattaccca caacgtgtct 1260
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aagttctgca aggacttctt tggctttatt ccgtctctcc tggggcatct gctcgaggaa 1380
cgccaagata ttaagaccaa aatgaaggag acccangatc cgattgaaaa aatactgctc 1440
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gctctagaat ttgtgaaata cattaactcg aagctccccg gtctcttgga gctcgaatat 1740
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gcggtactcc gtattctgga gggttttggc taccgtaagg aagacctccg ttagcaaaag 2280
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<210> 18

<211> 757

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:truncated
hybrid polymerase Hyb3

<220>

<221> MOD_RES

<222> (472)

<223> Xaa = unknown amino acid

<400> 18

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Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Gly Lys Pro Val Ile
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Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
      20              25              30

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Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
    35              40              45

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Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
 355 360 365

Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
 420 425 430
 Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg
755

<210> 19
<211> 2535
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
polymerase Sso7d fusion protein HyS4

<220>
<221> modified_base
<222> (1416)
<223> n = g, a, c or t

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ctgctggaag atgattctaa gattgatgaa gttagaaaaa tcaactgctga gcgccatggc 180
aagattgttc gtatcggttg tgcggaaaaag gtagagaaga aatttctggg cagaccaatc 240
acgggtgtgga aactgtatatt cgaacatcca caagatgttc cgactattcg cgagaaaaatt 300
cgcgaaacatt ctgcagttgt tggcatcttc gaatacgata ttccattttgc aaagagttac 360
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ccggatactc tcaaccgcga gggctgcaaa gactatgata ttgctccgga agtaggccac 1320
aagttctgca aggacttctt tggctttatt ccgtctctcc tggggcatct gctcgaggaa 1380
cgccaagaga ttaagaccaa aatgaaggag acccangatc cgattgaaaa aatactgctc 1440
gactatcgcc aaaaagcgat taaactcctt gcaaactctt attacggcta ttatggctat 1500
gcaaaagcac gctggtagtg taaggagtgt gctgagtcgg ttactgcttg gggtcgcgaa 1560
tacatcgagt tcgtgtggaa ggagctcgaa gaaaagtttg gctttaaaagt tctctacatt 1620
gacactgatg gtctctatgc gactattccg ggtggtgagc ctgaggaaat taagaaaaag 1680
gctctagaat ttgtgaaata cattaactcg aagctccccg gtctcttgga gctcgaatat 1740
gaaggctttt ataagcgcgg cttcttcggt accaagaaga gatatgcggt gattgatgaa 1800

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gaaggcaaaa ttattactcg tggctctcgag attgtgcgcc gtgattggag cgaaattgcg 1860
aaagaaactc aagctaaagt tctcgaggct attctcaaac acggcaacgt tgaagaagct 1920
gtgaaaattg taaaagaaat aatcgaaaag ctcgctaaat atgaaatacc gccagagaag 1980
ctcgcgattt atgagcagat tactcgcccc ctgcatgagt ataaggcgat tgggccgcac 2040
gtggctggtt caaagaaact ggctgctaga ggcgtgaaaa ttaaaccggg tatggtaatt 2100
ggctacattg tactccgcgg cgatgggtccg attagcaaac gtgcaattct agctgaggaa 2160
ttcgatccga aaaagcacaa gtatgacgca gaatattaca ttgagaacca ggtgctcccc 2220
gcggtactcc gtattctgga gggttttggc taccgtaagg aagacctccg ttggcaaaag 2280
actaaacagg ctggcctcac tgcttggctc aacattaaaa aatccggtac cggcgggtggc 2340
ggtgcaaccg taaagttcaa gtacaaaggc gaagaaaaag aggtagacat ctccaagatc 2400
aagaaagtat ggcgtgtggg caagatgac tccttcacct acgacgaggg cgggtggcaag 2460
accggccgtg gtgcggtaaag cgaaaaggac gcgccgaagg agctgctgca gatgctggag 2520
aagcagaaaa agtga 2535

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```

<210> 20
<211> 844
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein HyS4

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<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

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<400> 20
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1             5             10             15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
      20             25             30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
      35             40             45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
      50             55             60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
      65             70             75             80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
      85             90             95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
      100            105            110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
      115            120            125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
      130            135            140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
      145            150            155            160

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Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
 355 360 365
 Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
 420 425 430
 Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
805 810 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
820 825 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
835 840

<210> 21
<211> 189
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Sso7d coding
region

<400> 21
accgtaaagt tcaagtacaa aggcgaagaa aaagaggtag acatctccaa gatcaagaaa 60
gtatggcggtg tgggcaagat gatctccttc acctacgacg agggcggtgg caagaccggc 120
cgtggtgctg taagcgaaaa ggacgcgccg aaggagctgc tgcagatgct ggagaagcag 180
aaaaagtga 189

<210> 22
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Sso7d binding
domain

<400> 22
Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile
1 5 10 15
Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr
20 25 30
Tyr Asp Glu Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys
35 40 45
Asp Ala Pro Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
50 55 60

<210> 23
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:signature
invariable sequence element in hybrid polymerases
containing nucleotide binding motif

<400> 23
 Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys
 1 5 10 15
 Ala Glu Ser Val Thr Ala Trp Gly Arg
 20 25

 <210> 24
 <211> 775
 <212> PRT
 <213> Pyrococcus furiosus

 <220>
 <223> parent Pyrococcus furiosus family B DNA
 polymerase PolI (Pfu)

 <400> 24
 Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1 5 10 15
 Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
 20 25 30
 Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
 35 40 45
 Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
 65 70 75 80
 Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
 355 360 365
 Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
 385 390 395 400
 Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
 420 425 430
 Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
 625 630 635 640
 Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser
 770 775

<210> 25

<211> 775

<212> PRT

<213> Pyrococcus sp.

<220>

<223> parent Pyrococcus sp. strain GD-B PolI
 (Deep Vent) DNA polymerase

<400> 25

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
 1 5 10 15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Gln Ile
 35 40 45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60

Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80

Glu Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
 85 90 95

Arg Asp Lys Ile Arg Glu His Ser Ala Val Ile Asp Ile Phe Glu Tyr
 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
 145 150 155 160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190

Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Val Ile Ile Thr
 195 200 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu
 210 215 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
 245 250 255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
 260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285

Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
 290 295 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
 305 310 315 320

Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
 325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
 355 360 365
 Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Gly
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Glu Tyr
 420 425 430
 Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Glu Ile
 450 455 460
 Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
 465 470 475 480
 Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Ala Lys Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Lys Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ala
 755 760 765
 Trp Leu Asn Ile Lys Lys Lys
 770 775

<210> 26
 <211> 775
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:designed hybrid
 polymerase

<220>
 <221> MOD_RES
 <222> (1)..(775)
 <223> Xaa = unknown amino acid

<400> 26
 Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile
 1 5 10 15
 Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
 20 25 30
 Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
 35 40 45
 Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
 65 70 75 80
 Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile
 85 90 95
 Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125

Met	Glu	Gly	Xaa	Glu	Glu	Leu	Lys	Xaa	Leu	Ala	Phe	Asp	Ile	Glu	Thr	130	135	140
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Xaa	Lys	Gly	Pro	Ile	Ile	Met	Ile	145	150	155
Ser	Tyr	Ala	Asp	Glu	Xaa	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Xaa	Ile	165	170	175
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	180	185	190
Arg	Phe	Leu	Xaa	Xaa	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Xaa	Ile	Xaa	Thr	195	200	205
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Xaa	Pro	Tyr	Leu	Xaa	Lys	Arg	Ala	Glu	210	215	220
Lys	Leu	Gly	Ile	Lys	Leu	Xaa	Xaa	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235
Met	Gln	Arg	Xaa	Gly	Asp	Met	Thr	Ala	Val	Glu	Xaa	Lys	Gly	Arg	Ile	245	250	255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Xaa	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	275	280	285
Lys	Val	Tyr	Ala	Xaa	Glu	Ile	Ala	Xaa	Ala	Trp	Glu	Xaa	Gly	Xaa	Xaa	290	295	300
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Xaa	Thr	Tyr	305	310	315
Glu	Leu	Gly	Xaa	Glu	Phe	Xaa	Pro	Met	Glu	Xaa	Gln	Leu	Ser	Arg	Leu	325	330	335
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350
Val	Glu	Trp	Xaa	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Xaa	Ala	355	360	365
Pro	Asn	Lys	Pro	Xaa	Glu	Xaa	Glu	Tyr	Xaa	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380
Tyr	Xaa	Gly	Gly	Xaa	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Xaa	385	390	395
Xaa	Val	Xaa	Leu	Asp	Phe	Arg	Xaa	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410	415
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Xaa	Glu	Gly	Cys	Xaa	Xaa	Tyr	420	425	430
Asp	Xaa	Ala	Pro	Xaa	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Xaa	Pro	Gly	435	440	445

Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile
450 455 460
Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu
465 470 475 480
Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
515 520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540
Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu Glu Ile Lys Lys Lys
545 550 555 560
Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu
565 570 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys
580 585 590
Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly
595 600 605
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620
Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Xaa Val Glu Glu Ala
625 630 635 640
Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu Xaa Xaa Tyr Glu Ile
645 650 655
Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala
675 680 685
Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700
Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu
705 710 715 720
Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725 730 735
Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa
755 760 765

Trp Leu Asn Ile Lys Lys Ser
770 775

<210> 27
<211> 783
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:designed hybrid
polymerase from Figure 1

<220>
<221> MOD_RES
<222> (1)..(783)
<223> Xaa = unknown amino acid

<400> 27
Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile
1 5 10 15
Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
20 25 30
Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
35 40 45
Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
50 55 60
Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
65 70 75 80
Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile
85 90 95
Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr
100 105 110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125
Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr
130 135 140
Leu Tyr His Glu Gly Glu Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile
145 150 155 160
Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile
165 170 175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190
Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Xaa Pro Tyr Leu Xaa Lys Arg Ala Glu
210 215 220
Lys Leu Gly Ile Lys Leu Xaa Xaa Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240
Met Gln Arg Xaa Gly Asp Met Thr Ala Val Glu Xaa Lys Gly Arg Ile
245 250 255
His Phe Asp Leu Tyr His Val Ile Xaa Arg Thr Ile Asn Leu Pro Thr
260 265 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Xaa Glu Ile Ala Xaa Ala Trp Glu Xaa Gly Xaa Xaa
290 295 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Xaa Thr Tyr
305 310 315 320
Glu Leu Gly Xaa Glu Phe Xaa Pro Met Glu Xaa Gln Leu Ser Arg Leu
325 330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Xaa Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Xaa Ala
355 360 365
Pro Asn Lys Pro Xaa Glu Xaa Glu Tyr Xaa Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Xaa Gly Gly Xaa Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Xaa
385 390 395 400
Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr
420 425 430
Asp Xaa Ala Pro Xaa Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile
450 455 460
Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu
465 470 475 480
Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
515 520 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Xaa Val Glu Glu Ala
 625 630 635 640
 Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu Xaa Xaa Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala
 675 680 685
 Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr His Asn Cys Asn His Asp
 770 775 780

<210> 28

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase HyS1 from Figure 5

<220>
 <221> MOD_RES
 <222> (472)
 <223> Xaa = unknown amino acid

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 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile
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 Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
 20 25 30
 Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
 35 40 45
 Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Val Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Asp Lys Val Arg Glu His Pro Ala Val Ile Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Ala Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Gly Ser Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Thr Leu Gly Arg Asp Gly Cys Glu Ala Lys
 225 230 235 240
 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr Tyr Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285

Lys Val Tyr Ala Asp Asp Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
 355 360 365
 Pro Asn Lys Pro Tyr Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Ser
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
 420 425 430
 Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
 835 840 845

<210> 29
 <211> 758
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase Hyb2 from Figure 5

<220>
 <221> MOD_RES
 <222> (472)
 <223> Xaa = unknown amino acid

<400> 29

Met	Ile	Leu	Asp	Ala	Asp	Tyr	Ile	Thr	Glu	Glu	Gly	Lys	Pro	Val	Ile	
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Arg	Ile	Phe	Lys	Lys	Glu	Asn	Gly	Glu	Phe	Lys	Val	Glu	Tyr	Asp	Arg	
			20					25					30			
Asn	Phe	Arg	Pro	Tyr	Ile	Tyr	Ala	Leu	Leu	Glu	Asp	Asp	Ser	Lys	Ile	
		35					40					45				
Asp	Glu	Val	Arg	Lys	Ile	Thr	Ala	Glu	Arg	His	Gly	Lys	Ile	Val	Arg	
	50					55					60					
Ile	Val	Asp	Ala	Glu	Lys	Val	Glu	Lys	Lys	Phe	Leu	Gly	Arg	Pro	Ile	
65					70					75					80	
Thr	Val	Trp	Lys	Leu	Tyr	Phe	Glu	His	Pro	Gln	Asp	Val	Pro	Thr	Ile	
			85						90					95		
Arg	Glu	Lys	Ile	Arg	Glu	His	Ser	Ala	Val	Val	Gly	Ile	Phe	Glu	Tyr	
			100					105					110			
Asp	Ile	Pro	Phe	Ala	Lys	Ser	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	
		115					120					125				
Met	Glu	Gly	Glu	Glu	Glu	Leu	Lys	Leu	Leu	Ala	Phe	Asp	Ile	Glu	Thr	
	130					135					140					
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Ala	Lys	Gly	Pro	Ile	Ile	Met	Ile	
145					150					155					160	
Ser	Tyr	Ala	Asp	Glu	Asp	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Lys	Ile	
			165					170						175		
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	
			180					185					190			
Arg	Phe	Leu	Arg	Val	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Val	Ile	Val	Thr	
		195					200					205				
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Leu	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu	
	210					215					220					
Lys	Leu	Gly	Ile	Lys	Leu	Pro	Leu	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	
225					230					235					240	
Met	Gln	Arg	Leu	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	
			245					250						255		
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Ser	Arg	Thr	Ile	Asn	Leu	Pro	Thr	
		260						265					270			
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	
		275					280					285				
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Gly	Ala	Trp	Glu	Thr	Gly	Glu	Asp	
	290					295					300					
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Ile	Tyr	
305					310					315					320	

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
 355 360 365
 Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
 420 425 430
 Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Asn
 755

<210> 30
 <211> 758
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase Hyb3 from Figure 5

<220>
 <221> MOD_RES
 <222> (472)
 <223> Xaa = unknown amino acid

<400> 30
 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1 5 10 15
 Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
 35 40 45
 Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
 100 105 110

Asp	Ile	Pro	Phe	Ala	Lys	Ser	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	115	120	125
Met	Glu	Gly	Glu	Glu	Glu	Leu	Lys	Leu	Leu	Ala	Phe	Asp	Ile	Glu	Thr	130	135	140
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Ala	Lys	Gly	Pro	Ile	Ile	Met	Ile	145	150	155
Ser	Tyr	Ala	Asp	Glu	Asp	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Lys	Ile	165	170	175
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	180	185	190
Arg	Phe	Leu	Arg	Val	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Val	Ile	Val	Thr	195	200	205
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Leu	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu	210	215	220
Lys	Leu	Gly	Ile	Lys	Leu	Pro	Leu	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235
Met	Gln	Arg	Leu	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	245	250	255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Ser	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	275	280	285
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Gly	Ala	Trp	Glu	Thr	Gly	Glu	Asp	290	295	300
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Ile	Tyr	305	310	315
Glu	Leu	Gly	Lys	Glu	Phe	Phe	Pro	Met	Glu	Val	Gln	Leu	Pro	Arg	Leu	325	330	335
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350
Val	Glu	Trp	Leu	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Leu	Ala	355	360	365
Pro	Asn	Lys	Pro	Ala	Glu	Gln	Glu	Tyr	Glu	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380
Tyr	Thr	Gly	Gly	Phe	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asp	385	390	395
Leu	Val	Ser	Leu	Asp	Phe	Arg	Ala	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410	415
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Lys	Asp	Tyr	420	425	430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Asn
755

<210> 31
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
polymerase HyS4 from Figure 5

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 31
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
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Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
20 25 30
Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
35 40 45
Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60
Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80
Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95
Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
100 105 110
Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125
Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
130 135 140
Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145 150 155 160
Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
165 170 175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190
Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220
Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240
Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255
His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
260 265 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
290 295 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305 310 315 320
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
325 330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365
Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385 390 395 400
Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
420 425 430
Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
435 440 445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
450 455 460
Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
515 520 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
 835 840 845

<210> 32
 <211> 845
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase PhS1 from Figure 5

<400> 32
 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
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 Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu His Asp Arg
 20 25 30
 Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
 35 40 45
 Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
 260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Thr Gly Glu Gly
290 295 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
325 330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365
Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Ala Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400
Ile Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
420 425 430
Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Lys Ile
450 455 460
Lys Thr Lys Met Lys Ala Ser Gln Asp Pro Ile Glu Lys Ile Met Leu
465 470 475 480
Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
515 520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540
Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545 550 555 560
Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
565 570 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580 585 590

Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ser Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Pro Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
 835 840 845

<210> 33

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase PhS2 from Figure 5

<400> 33

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
 35 40 45
 Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Lys Pro Ile
 65 70 75 80
 Glu Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Ser Gly Glu Gly
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ile Gln Leu Ser Arg Leu
 325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365
Pro Asn Lys Pro Ser Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400
Ile Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Glu Tyr
420 425 430
Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
450 455 460
Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480
Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu
515 520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540
Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545 550 555 560
Ala Leu Glu Phe Val Asp Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565 570 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580 585 590
Lys Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
595 600 605
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620
Ala Lys Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala
625 630 635 640
Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Pro Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Tyr Gln Lys Thr Lys Gln Val Asp Leu Thr Ala
 755 760 765
 Cys Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu 'Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
 835 840 845

<210> 34
 <211> 145
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase PhS3 from Figure 5

<400> 34
 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Ile Ile
 1 5 10 15
 Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
 35 40 45
 Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
 65 70 75 80

Glu	Val	Trp	Lys	Leu	Tyr	Leu	Glu	His	Pro	Gln	Asp	Val	Pro	Thr	Ile
			85						90					95	
Arg	Glu	Lys	Ile	Arg	Glu	His	Ser	Ala	Val	Val	Asp	Ile	Phe	Glu	Tyr
			100					105					110		
Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro
		115					120					125			
Met	Glu	Gly	Val	Arg	Tyr	Arg	Asn	Pro	Leu	Ser	Arg	Arg	Arg	Arg	Val
	130					135					140				

Trp
145

<210> 35
 <211> 844
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase PhS4 from Figure 5

<400> 35

Met	Ile	Leu	Asp	Ala	Asp	Tyr	Ile	Thr	Glu	Glu	Gly	Lys	Pro	Val	Ile
1				5					10					15	
Arg	Leu	Phe	Lys	Lys	Glu	Asn	Gly	Glu	Phe	Lys	Val	Glu	Tyr	Asp	Arg
			20				25						30		
Asn	Phe	Arg	Pro	Tyr	Ile	Tyr	Ala	Leu	Leu	Arg	Asp	Asp	Ser	Gln	Ile
		35					40				45				
Asp	Glu	Val	Arg	Lys	Ile	Thr	Gly	Glu	Arg	His	Gly	Lys	Ile	Val	Arg
	50					55					60				
Ile	Val	Asp	Ala	Glu	Lys	Val	Glu	Lys	Lys	Phe	Leu	Gly	Arg	Pro	Ile
65					70					75					80
Glu	Val	Trp	Lys	Leu	Tyr	Leu	Glu	His	Pro	Gln	Asp	Val	Pro	Ala	Ile
			85						90					95	
Arg	Glu	Lys	Val	Arg	Glu	His	Ser	Ala	Val	Val	Asp	Ile	Phe	Glu	Tyr
			100					105					110		
Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro
		115					120					125			
Met	Glu	Gly	Glu	Glu	Glu	Leu	Lys	Leu	Leu	Ala	Phe	Asp	Ile	Glu	Thr
	130					135					140				
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Ala	Lys	Gly	Pro	Ile	Ile	Met	Ile
145					150					155					160
Ser	Tyr	Ala	Asp	Glu	Asn	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Lys	Ile
			165						170					175	
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys
			180					185					190		

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala His Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Gly
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
 355 360 365
 Pro Asn Lys Pro Ser Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
 385 390 395 400
 Ile Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asn Tyr
 420 425 430
 Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Lys Ile
 450 455 460
 Lys Arg Lys Met Lys Glu Ser Gln Asp Pro Ile Glu Lys Lys Met Leu
 465 470 475 480
 Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Gly Leu
 530 535 540
 Tyr Ala Thr Ile Pro Gly Ala Lys Ser Glu Glu Ile Lys Lys Lys Ala
 545 550 555 560
 Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu Glu
 565 570 575
 Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys
 580 585 590
 Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu
 595 600 605
 Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
 610 615 620
 Arg Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala Val
 625 630 635 640
 Arg Ile Val Lys Glu Val Thr Lys Lys Leu Ser Asn Tyr Glu Ile Pro
 645 650 655
 Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu
 660 665 670
 Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala
 675 680 685
 Lys Gly Val Lys Ile Arg Pro Gly Met Val Ile Gly Tyr Ile Val Leu
 690 695 700
 Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Tyr
 705 710 715 720
 Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln
 725 730 735
 Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg Lys
 740 745 750
 Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ala Trp
 755 760 765
 Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val Lys
 770 775 780
 Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
 785 790 795 800
 Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
 805 810 815

Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
820 825 830

Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
835 840

<210> 36

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase PhS5 from Figure 5

<400> 36

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
35 40 45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
85 90 95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240

Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Ile	Lys	Gly	Arg	Ile		
				245					250					255			
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Thr	Arg	Thr	Ile	Asn	Leu	Pro	Thr		
			260					265					270				
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu		
		275					280					285					
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Glu	Ala	Trp	Glu	Ser	Gly	Lys	Asn		
	290					295					300						
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr		
305					310					315					320		
Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ile	Gln	Leu	Ser	Arg	Leu		
				325					330					335			
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu		
			340					345					350				
Val	Glu	Trp	Tyr	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Val	Ala		
		355					360					365					
Pro	Asn	Lys	Pro	Asp	Glu	Glu	Glu	Tyr	Glu	Arg	Arg	Leu	Arg	Glu	Ser		
	370					375					380						
Tyr	Thr	Gly	Gly	Tyr	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asn		
385					390					395					400		
Leu	Val	Ser	Leu	Asp	Phe	Arg	Ala	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr		
				405					410						415		
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Lys	Glu	Tyr		
			420					425					430				
Asp	Ile	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Pro	Gly		
	435						440					445					
Phe	Ile	Pro	Ser	Leu	Leu	Lys	His	Leu	Leu	Asp	Glu	Arg	Gln	Glu	Ile		
	450					455					460						
Lys	Arg	Lys	Met	Lys	Ala	Ser	Lys	Asp	Pro	Ile	Glu	Lys	Lys	Met	Leu		
465					470					475					480		
Asp	Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Phe	Tyr	Gly		
				485					490					495			
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu		
			500					505					510				
Ser	Val	Thr	Ala	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Leu	Val	Trp	Lys	Glu		
			515				520					525					
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly		
	530					535					540						
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Lys	Pro	Glu	Glu	Ile	Lys	Lys	Lys		
545					550					555					560		

Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu	565	570	575
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Val	Arg	Gly	Phe	Phe	Val	Thr	Lys	580	585	590
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Ile	Ile	Thr	Arg	Gly	595	600	605
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	610	615	620
Ala	Arg	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asn	Val	Glu	Glu	Ala	625	630	635
Val	Lys	Ile	Val	Lys	Glu	Val	Thr	Gln	Lys	Leu	Ala	Lys	Tyr	Glu	Ile	645	650	655
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His	660	665	670
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Arg	Leu	Ala	675	680	685
Ala	Arg	Gly	Val	Lys	Val	Arg	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val	690	695	700
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu	705	710	715
Tyr	Asp	Leu	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn	725	730	735
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Ala	Phe	Gly	Tyr	Arg	740	745	750
Lys	Glu	Asp	Leu	Arg	Trp	Gln	Lys	Thr	Lys	Gln	Val	Gly	Leu	Thr	Ser	755	760	765
Trp	Leu	Asn	Ile	Lys	Lys	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Ala	Thr	Val	770	775	780
Lys	Phe	Lys	Tyr	Lys	Gly	Glu	Glu	Lys	Glu	Val	Asp	Ile	Ser	Lys	Ile	785	790	795
Lys	Lys	Val	Trp	Arg	Val	Gly	Lys	Met	Ile	Ser	Phe	Thr	Tyr	Asp	Glu	805	810	815
Gly	Gly	Gly	Lys	Thr	Gly	Arg	Gly	Ala	Val	Ser	Glu	Lys	Asp	Ala	Pro	820	825	830
Lys	Glu	Leu	Leu	Gln	Met	Leu	Glu	Lys	Gln	Lys	Lys	Asn				835	840	845

<210> 37
 <211> 472
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase PhS6 from Figure 5

<400> 37

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Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
  1             5             10             15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
      20             25             30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
      35             40             45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
      50             55             60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
      65             70             75             80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
      85             90             95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
      100            105            110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
      115            120            125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
      130            135            140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
      145            150            155            160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
      165            170            175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
      180            185            190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
      195            200            205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
      210            215            220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
      225            230            235            240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
      245            250            255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
      260            265            270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
      275            280            285

Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
      290            295            300
```

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
 355 360 365
 Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr
 420 425 430
 Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Glu Glu Arg Gln Lys Ile
 450 455 460
 Lys Arg Lys Met Lys Ala Thr Asn
 465 470

<210> 38
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:region
 containing invariable sequence element from
 parental Pfu polymerase containing nucleotide
 binding motif

<400> 38
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
 1 5 10 15
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 20 25 30
 Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
 35 40 45
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
 50 55 60

<210> 39
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:region
 containing invariable sequence element from
 parental Deep Vent polymerase containing
 nucleotide binding motif

<400> 39
 Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
 1 5 10 15
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 20 25 30
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
 35 40 45
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
 50 55 60

<210> 40
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:region
 containing invariable sequence element from
 dedigned hybrid polymerase containing nucleotide
 binding motif

<220>
 <221> MOD_RES
 <222> (1)..(60)
 <223> Xaa = unknown amino acid

<400> 40
 Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
 1 5 10 15
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 20 25 30
 Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
 35 40 45
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
 50 55 60

<210> 41
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:region
 containing invariable sequence elements from HyS1,
 Hyb2, Hyb3 and HyS4 hybrid polymerase containing
 nucleotide binding motif

<400> 41
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 1 5 10 15
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 20 25 30
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
 35 40 45
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
 50 55 60

<210> 42
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:region
 containing invariable sequence element from PhS1
 hybrid polymerase containing nucleotide binding
 motif

<400> 42
 Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
 1 5 10 15
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 20 25 30
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
 35 40 45
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
 50 55 60

<210> 43
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:region
 containing invariable sequence element from PhS2
 hybrid polymerase containing nucleotide binding
 motif

<400> 43
 Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
 1 5 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
20 25 30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu
35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
50 55 60

<210> 44
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
containing invariable sequence element from PhS4
hybrid polymerase containing nucleotide binding
motif

<400> 44
Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
1 5 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
20 25 30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
50 55 60

<210> 45
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region
containing invariable sequence element from PhS5
hybrid polymerase containing nucleotide binding
motif

<400> 45
Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
1 5 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
20 25 30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu
35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
50 55 60

<210> 46
<211> 60
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:region
containing invariable sequence element from PhS7
hybrid polymerase containing nucleotide binding
motif

<400> 46

Asp Tyr Arg Gln Lys Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly
1 5 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
20 25 30

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Phe Val Arg Lys Glu
35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
50 55 60

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:6-His
polyhistidine epitope tag, metal chelate affinity
ligand

<400> 47

His His His His His His
1 5

<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:anti-DYKDDDDK
epitope tag

<400> 48

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 49
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer to
 measure exonuclease activity

 <220>
 <221> modified_base
 <222> (1)
 <223> n = t modified by 6-carboxy-fluorescein (FAM)

 <220>
 <221> modified_base
 <222> (45)
 <223> n = t amino-linked to quencher
 4-(4-dimethylaminophenylazo)benzoyl group (dabcyl,
 DAB)

 <400> 49
 ntttttgagg tgtgtcctac acagcggagt gtaggacaca cctcn

45